Amendments to the Specification

Please replace paragraph [0028] of the originally filed specification with the following new paragraph:

[0028] A number of analytical methods have been developed which can locate or identify SNPs. One exemplary method involves sample amplification using pairs of fluorescent probes wherein each probe comprises a discrete marker or reporter dye specific for a different allele. During amplification the sample is labeled according to its particular allelic composition and the fluorescent properties of the resulting product can be evaluated to determine if the sample is homozygous for a first allele (e.g. A/A), ~~homozygous for a second allele~~ a heterozygous allelic combination (e.g. A/B), or ~~a heterozygous allelic combination~~ homozygous for a second allele (e.g. B/B). Homozygous samples tend to exhibit an increased degree of fluorescence in one or the other marker type with the amount of observed fluorescence from the opposing marker being significantly diminished or completely absent. Conversely, a sample heterozygous for both alleles typically exhibits a substantial degree of fluorescence arising from both markers. A commercial implementation of this method is Applied Biosystems' Taqman platform, which employs Applied Biosystems' Prism 7700 and 7900HT sequence detection systems to monitor and record the fluorescence of each amplified sample.